

10/571667

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Substitute Sequence Listing

<110> DE VRIES, Erik
GAFFAR, Fasilla Razzia
YATSUDA, Ana Patricia
SCHAAP, Theodorus Cornelis

<120> Piroplasmid vaccine

<130> I-2003.010 US

<140>

<141>

<150> PCT/EP2004/052169

<151> 2004-09-14

<150> EP 03020898.7

<151> 2003-09-14

<160> 20

<170> PatentIn version 3.3

<210> 1

<211> 1818

<212> DNA

<213> Babesia bovis

<220>

<221> CDS

<222> (1)...(1818)

<400> 1

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Met Gln Leu His Asn Lys Met Gln Ser Thr Ser Leu Lys Tyr Asn Tyr
1 5 10 15

aag cgc atg ctt tgt atg gct ctt gta cca gtt atc tta tcg tca ttt 96
Lys Arg Met Leu Cys Met Ala Leu Val Pro Val Ile Leu Ser Ser Phe
20 25 30

ttt gcg gaa gat gct tta gct tcc aac tcc acg ctt ttc gct ttc cac 144
Phe Ala Glu Asp Ala Leu Ala Ser Asn Ser Thr Leu Phe Ala Phe His
35 40 45

aag gaa cca aac aat cgt agg ctt acc aaa agg tct tca aga gga cag 192
Lys Glu Pro Asn Asn Arg Arg Leu Thr Lys Arg Ser Ser Arg Gly Gln
50 55 60

ttg ctc aac tca agg agg ggt tcg gat gat gcg tcc gaa tct tcc gat 240
Leu Leu Asn Ser Arg Arg Gly Ser Asp Asp Ala Ser Glu Ser Ser Asp
65 70 75 80

aga tac cca ggt agg tcg ggt ggc tct aag aat tcg agc caa tcc ccc 288
Arg Tyr Pro Gly Arg Ser Gly Ser Lys Asn Ser Ser Gln Ser Pro
85 90 95

tgg atc aag tat atg caa aag ttc gac att ccc cgt aac cac ggc tct 336
Trp Ile Lys Tyr Met Gln Lys Phe Asp Ile Pro Arg Asn His Gly Ser
100 105 110

Substitute Sequence Listing

gga atc tat gtc gat ctt gga gga tat gaa tcc gtt ggt tca aaa agt Gly Ile Tyr Val Asp Leu Gly Gly Tyr Glu Ser Val Gly Ser Lys Ser 115 120 125	384
tat cgt atg ccc gtt ggt aag tgc cca gta gtc ggt aaa att ata gac Tyr Arg Met Pro Val Gly Lys Cys Pro Val Val Gly Lys Ile Ile Asp 130 135 140	432
ctt gga aat ggt gcc gac ttc ctc gat ccc att tca tca gac gac cca Leu Gly Asn Gly Ala Asp Phe Leu Asp Pro Ile Ser Ser Asp Asp Pro 145 150 155 160	480
agt tac cgt ggt ttg gca ttc ccc gag act gct gtg gac tct aat att Ser Tyr Arg Gly Leu Ala Phe Pro Glu Thr Ala Val Asp Ser Asn Ile 165 170 175	528
ccc aca caa cca aag aca cgt ggt tct tca tca gca tct gcg gcc aaa Pro Thr Gln Pro Lys Thr Arg Gly Ser Ser Ser Ala Ser Ala Ala Lys 180 185 190	576
tta tct cct gtt tcg gcg aaa gat ctg aga cgt tgg gga tat gaa ggt Leu Ser Pro Val Ser Ala Lys Asp Leu Arg Arg Trp Gly Tyr Glu Gly 195 200 205	624
aat gat gta gcg aat tgc tca gaa tat gct agt aac ctc att ccc gca Asn Asp Val Ala Asn Cys Ser Glu Tyr Ala Ser Asn Leu Ile Pro Ala 210 215 220	672
tca gac agg agt acc aaa tat agg tat cct ttt gtt ttt gac agt gat Ser Asp Arg Ser Thr Lys Tyr Arg Tyr Pro Phe Val Phe Asp Ser Asp 225 230 235 240	720
aac cag atg tgt tac ata ctg tac tct gcc ata caa tac aac caa gga Asn Gln Met Cys Tyr Ile Leu Tyr Ser Ala Ile Gln Tyr Asn Gln Gly 245 250 255	768
aat agg tat tgt gac aac gat ggt agc tcc gaa gat ggt aca agc tct Asn Arg Tyr Cys Asp Asn Asp Gly Ser Ser Glu Asp Gly Thr Ser Ser 260 265 270	816
ttg ctt tgc atg aaa cct tac aag agc gct gag gat gca cac tta tac Leu Leu Cys Met Lys Pro Tyr Lys Ser Ala Glu Asp Ala His Leu Tyr 275 280 285	864
tac ggt tct gcg aaa gtt gac ccc gat tgg gaa gaa aat tgt ccc atg Tyr Gly Ser Ala Lys Val Asp Pro Asp Trp Glu Glu Asn Cys Pro Met 290 295 300	912
cac ccg gta agg gat gcc att ttt ggt aaa tgg tct ggt ggc tct tgt His Pro Val Arg Asp Ala Ile Phe Gly Lys Trp Ser Gly Gly Ser Cys 305 310 315 320	960
gtt gcc att gct cct gca ttc caa gaa tat gcc aac agc act gaa gac Val Ala Ile Ala Pro Ala Phe Gln Glu Tyr Ala Asn Ser Thr Glu Asp 325 330 335	1008
tgt gca gcc att tta ttc gat aac tct gca act gac ttg aat atc gaa Cys Ala Ala Ile Leu Phe Asp Asn Ser Ala Thr Asp Leu Asn Ile Glu 340 345 350	1056
gct gtt aac gaa gat ttt aat gaa ctt aaa gaa ttg acc gat ggg ctt Ala Val Asn Glu Asp Phe Asn Glu Leu Lys Glu Leu Thr Asp Gly Leu	1104

355

Substitute Sequence Listing
360 365

1152

aaa aga ttg aac atg tcg aag gtt gca aac gct att ttt tct ccc ctc
Lys Arg Leu Asn Met Ser Lys Val Ala Asn Ala Ile Phe Ser Pro Leu
370 375 380

1200

tcc aat gtt gca ggt acc agt cga att tca cgt ggt gtg ggt atg aac
Ser Asn Val Ala Gly Thr Ser Arg Ile Ser Arg Gly Val Gly Met Asn
385 390 395 400

1248

tgg gct aca tac gat aaa gat tct ggt atg tgt gct ctc att aac gaa
Trp Ala Thr Tyr Asp Lys Asp Ser Gly Met Cys Ala Leu Ile Asn Glu
405 410 415

1296

aca cct aac tgc ttg atc ttg aac gcg gga agc att gct ctc acg gct
Thr Pro Asn Cys Leu Ile Leu Asn Ala Gly Ser Ile Ala Leu Thr Ala
420 425 430

1344

ata ggt tca cct ctc gag tat gac gct gtt aac tat cct tgc cac atc
Ile Gly Ser Pro Leu Glu Tyr Asp Ala Val Asn Tyr Pro Cys His Ile
435 440 445

1392

gac acc aat ggt tac gtt gag cca cgt gca aag aat acc aac aaa tac
Asp Thr Asn Gly Tyr Val Glu Pro Arg Ala Lys Asn Thr Asn Lys Tyr
450 455 460

1440

ctt gat gtt cct ttc gag gtc aca act gct ttg agc atg aag aca cta
Leu Asp Val Pro Phe Glu Val Thr Thr Ala Leu Ser Met Lys Thr Leu
465 470 475 480

1488

aaa tgc gat gcc tat gtt cac acc aag tac tct gac agt tgt ggt acc
Lys Cys Asp Ala Tyr Val His Thr Lys Tyr Ser Asp Ser Cys Gly Thr
485 490 495

1536

tat ttc ctt tgc tca gac gtc aaa cct aac tgg ttc att agg ttc tta
Tyr Phe Leu Cys Ser Asp Val Lys Pro Asn Trp Phe Ile Arg Phe Leu
500 505 510

1584

cac atg atc gga ctc tac aac aca aag cgt atc gta ata ttc gtg tgc
His Met Ile Gly Leu Tyr Asn Thr Lys Arg Ile Val Ile Phe Val Cys
515 520 525

1632

tgt acc act acc gcc atc gtt ctc act atc tgg ata tgg aaa cga ttc
Cys Thr Thr Ala Ile Val Leu Thr Ile Trp Ile Trp Lys Arg Phe
530 535 540

1680

atc aag gct aag aaa gag ccg gcc cct cca agt ttc gac aaa tac cta
Ile Lys Ala Lys Lys Glu Pro Ala Pro Pro Ser Phe Asp Lys Tyr Leu
545 550 555 560

1728

agc aac tat gat tat gat aca acc cta gat gcc gac aac gaa acg gaa
Ser Asn Tyr Asp Tyr Asp Thr Thr Leu Asp Ala Asp Asn Glu Thr Glu
565 570 575

1776

cag cgt ttg gat tcc tct gct tat agc tgg gga gag gct gta caa aga
Gln Arg Leu Asp Ser Ser Ala Tyr Ser Trp Gly Glu Ala Val Gln Arg
580 585 590

1818

cca agt gat gtc acc cct gta aaa ctc tct aaa atc aac taa
Pro Ser Asp Val Thr Pro Val Lys Leu Ser Lys Ile Asn
595 600 605

Substitute Sequence Listing

<210> 2
<211> 605
<212> PRT
<213> Babesia bovis

<400> 2

Met Gln Leu His Asn Lys Met Gln Ser Thr Ser Leu Lys Tyr Asn Tyr
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Lys Arg Met Leu Cys Met Ala Leu Val Pro Val Ile Leu Ser Ser Phe
20 25 30

Phe Ala Glu Asp Ala Leu Ala Ser Asn Ser Thr Leu Phe Ala Phe His
35 40 45

Lys Glu Pro Asn Asn Arg Arg Leu Thr Lys Arg Ser Ser Arg Gly Gln
50 55 60

Leu Leu Asn Ser Arg Arg Gly Ser Asp Asp Ala Ser Glu Ser Ser Asp
65 70 75 80

Arg Tyr Pro Gly Arg Ser Gly Ser Lys Asn Ser Ser Gln Ser Pro
85 90 95

Trp Ile Lys Tyr Met Gln Lys Phe Asp Ile Pro Arg Asn His Gly Ser
100 105 110

Gly Ile Tyr Val Asp Leu Gly Gly Tyr Glu Ser Val Gly Ser Lys Ser
115 120 125

Tyr Arg Met Pro Val Gly Lys Cys Pro Val Val Gly Lys Ile Ile Asp
130 135 140

Leu Gly Asn Gly Ala Asp Phe Leu Asp Pro Ile Ser Ser Asp Asp Pro
145 150 155 160

Ser Tyr Arg Gly Leu Ala Phe Pro Glu Thr Ala Val Asp Ser Asn Ile
165 170 175

Pro Thr Gln Pro Lys Thr Arg Gly Ser Ser Ser Ala Ser Ala Ala Lys
180 185 190

Leu Ser Pro Val Ser Ala Lys Asp Leu Arg Arg Trp Gly Tyr Glu Gly
195 200 205

Asn Asp Val Ala Asn Cys Ser Glu Tyr Ala Ser Asn Leu Ile Pro Ala
210 215 220

Substitute Sequence Listing

Ser Asp Arg Ser Thr Lys Tyr Arg Tyr Pro Phe Val Phe Asp Ser Asp
225 230 235 240

Asn Gln Met Cys Tyr Ile Leu Tyr Ser Ala Ile Gln Tyr Asn Gln Gly
245 250 255

Asn Arg Tyr Cys Asp Asn Asp Gly Ser Ser Glu Asp Gly Thr Ser Ser
260 265 270

Leu Leu Cys Met Lys Pro Tyr Lys Ser Ala Glu Asp Ala His Leu Tyr
275 280 285

Tyr Gly Ser Ala Lys Val Asp Pro Asp Trp Glu Glu Asn Cys Pro Met
290 295 300

His Pro Val Arg Asp Ala Ile Phe Gly Lys Trp Ser Gly Gly Ser Cys
305 310 315 320

Val Ala Ile Ala Pro Ala Phe Gln Glu Tyr Ala Asn Ser Thr Glu Asp
325 330 335

Cys Ala Ala Ile Leu Phe Asp Asn Ser Ala Thr Asp Leu Asn Ile Glu
340 345 350

Ala Val Asn Glu Asp Phe Asn Glu Leu Lys Glu Leu Thr Asp Gly Leu
355 360 365

Lys Arg Leu Asn Met Ser Lys Val Ala Asn Ala Ile Phe Ser Pro Leu
370 375 380

Ser Asn Val Ala Gly Thr Ser Arg Ile Ser Arg Gly Val Gly Met Asn
385 390 395 400

Trp Ala Thr Tyr Asp Lys Asp Ser Gly Met Cys Ala Leu Ile Asn Glu
405 410 415

Thr Pro Asn Cys Leu Ile Leu Asn Ala Gly Ser Ile Ala Leu Thr Ala
420 425 430

Ile Gly Ser Pro Leu Glu Tyr Asp Ala Val Asn Tyr Pro Cys His Ile
435 440 445

Asp Thr Asn Gly Tyr Val Glu Pro Arg Ala Lys Asn Thr Asn Lys Tyr
450 455 460

Leu Asp Val Pro Phe Glu Val Thr Thr Ala Leu Ser Met Lys Thr Leu
465 470 475 480

Substitute Sequence Listing

Lys Cys Asp Ala Tyr Val His Thr Lys Tyr Ser Asp Ser Cys Gly Thr
 485 490 495

Tyr Phe Leu Cys Ser Asp Val Lys Pro Asn Trp Phe Ile Arg Phe Leu
 500 505 510

His Met Ile Gly Leu Tyr Asn Thr Lys Arg Ile Val Ile Phe Val Cys
 515 520 525

Cys Thr Thr Thr Ala Ile Val Leu Thr Ile Trp Ile Trp Lys Arg Phe
 530 535 540

Ile Lys Ala Lys Lys Glu Pro Ala Pro Pro Ser Phe Asp Lys Tyr Leu
 545 550 555 560

Ser Asn Tyr Asp Tyr Asp Thr Thr Leu Asp Ala Asp Asn Glu Thr Glu
 565 570 575

Gln Arg Leu Asp Ser Ser Ala Tyr Ser Trp Gly Glu Ala Val Gln Arg
 580 585 590

Pro Ser Asp Val Thr Pro Val Lys Leu Ser Lys Ile Asn
 595 600 605

<210> 3
 <211> 2349
 <212> DNA
 <213> Theileria annulata

<220>
 <221> CDS
 <222> (1)..(2349)

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1 5 10 15		
cct gtg tta gga agc aac tct gac cct tcg gaa gag tat gat tca ttc		96
Pro Val Leu Gly Ser Asn Ser Asp Pro Ser Glu Glu Tyr Asp Ser Phe		
20 25 30		
cag caa aat gtt ttc act cat caa cca acc caa cta cac aaa tct cat		144
Gln Gln Val Phe Thr His Gln Pro Thr Gln Leu His Lys Ser His		
35 40 45		
cac tac att aca cac cag aaa aaa acc agc caa cac atc gac gat tta		192
His Tyr Ile Thr His Gln Lys Lys Thr Ser Gln His Ile Asp Asp Leu		
50 55 60		
aat ttt tat aat gga aaa ttt aat caa aag agc aga att ggt cca ggg		240
Asn Phe Tyr Asn Gly Lys Phe Asn Gln Lys Ser Arg Ile Gly Pro Gly		
65 70 75 80		

Substitute Sequence Listing

aag gta gta aat aac agt agg aat ctg gta gaa ggt gaa aca cta tct Lys Val Val Asn Asn Ser Arg Asn Leu Val Glu Gly Glu Thr Leu Ser 85 90 95	288
aag gat gac aat aaa aca aaa tct aaa ata aag tca aaa aca gca tca Lys Asp Asp Asn Lys Thr Lys Ser Lys Ile Lys Ser Lys Thr Ala Ser 100 105 110	336
att tta cct aga ctt tta aaa tct tta tca ttt tta gct gtt tta ggg Ile Leu Pro Arg Leu Leu Lys Ser Leu Ser Phe Leu Ala Val Leu Gly 115 120 125	384
tca att aat tca ttt tca tta gca tta gag gaa cct ttt act caa cac Ser Ile Asn Ser Phe Ser Leu Ala Leu Glu Glu Pro Phe Thr Gln His 130 135 140	432
act tct aac cga acg ccc ttt gaa gta tca tta att caa agc aac agc Thr Ser Asn Arg Thr Pro Phe Glu Val Ser Leu Ile Gln Ser Asn Ser 145 150 155 160	480
agt tta tcg cct att cat aat tct tca act caa aat tca agt cat cac Ser Leu Ser Pro Ile His Asn Ser Ser Thr Gln Asn Ser Ser His His 165 170 175	528
aac ggt ttt agt ggt agt acc gtt aat aat acc tca tta ata gag aca Asn Gly Phe Ser Gly Ser Thr Val Asn Asn Thr Ser Leu Ile Glu Thr 180 185 190	576
agg aat aac gta tta aac aga aca cta ggt aga ttc gga tca ttt ttg Arg Asn Asn Val Leu Asn Arg Thr Leu Gly Arg Phe Gly Ser Phe Leu 195 200 205	624
caa tca gga ttg ata agc agt aga gca gac aaa aag aag cgg tct ggt Gln Ser Gly Leu Ile Ser Ser Arg Ala Asp Lys Lys Lys Arg Ser Gly 210 215 220	672
atg aat aga aga ggc cct aag ggg aag aaa ggg aag gga gga gaa gac Met Asn Arg Arg Gly Pro Lys Gly Lys Lys Gly Lys Gly Glu Asp 225 230 235 240	720
gaa gaa aag agg aac aag tgg acc gat ttc atg gca aag ttt gat atc Glu Glu Lys Arg Asn Lys Trp Thr Asp Phe Met Ala Lys Phe Asp Ile 245 250 255	768
gct aag gtc cac ggt tca ggg gtt tac gta gat ttg ggt gaa tct gcc Ala Lys Val His Gly Ser Gly Val Tyr Val Asp Leu Gly Glu Ser Ala 260 265 270	816
acc gtt ggc agt tat gac tac agg atg cct ata gga aaa tgt cca gtt Thr Val Gly Ser Tyr Asp Tyr Arg Met Pro Ile Gly Lys Cys Pro Val 275 280 285	864
gta ggt aag gca atc ata ctc gag aat gga gct gat ttt ttg agc agc Val Gly Lys Ala Ile Ile Leu Glu Asn Gly Ala Asp Phe Leu Ser Ser 290 295 300	912
ata acc cat cat gac ccc aag gag aga ggg ctg ggg ttc cct gct aca Ile Thr His His Asp Pro Lys Glu Arg Gly Leu Gly Phe Pro Ala Thr 305 310 315 320	960
aaa gtt gcc tca aat tca tca aaa ctg gac atg gag aac cag ctc tta Lys Val Ala Ser Asn Ser Ser Lys Leu Asp Met Glu Asn Gln Leu Leu	1008

Substitute Sequence Listing

325

330

335

tca cca att agt gct cag gtc cta agg agc tgg aat tat aaa cac gaa Ser Pro Ile Ser Ala Gln Val Leu Arg Ser Trp Asn Tyr Lys His Glu 340 345 350	1056
tca gat tta agt aat tgt gct gag tat tcg aga aac att gtt ccg ggc Ser Asp Leu Ser Asn Cys Ala Glu Tyr Ser Arg Asn Ile Val Pro Gly 355 360 365	1104
agt aat cgt aat tca aag tat cgt tac ccg ttt gta tat gat gag tct Ser Asn Arg Asn Ser Lys Tyr Arg Tyr Pro Phe Val Tyr Asp Glu Ser 370 375 380	1152
gag aag ctt tgt tat att tta tat agt ccc atg caa tat aat cag ggc Glu Lys Leu Cys Tyr Ile Leu Tyr Ser Pro Met Gln Tyr Asn Gln Gly 385 390 395 400	1200
gta aag tac tgt gac caa gac tct ccg gac gaa gga act agc agt tta Val Lys Tyr Cys Asp Gln Asp Ser Pro Asp Glu Gly Thr Ser Ser Leu 405 410 415	1248
gct tgt atg tac ccg gat aag agc aag gag gat tca cac cta ttt tac Ala Cys Met Tyr Pro Asp Lys Ser Lys Glu Asp Ser His Leu Phe Tyr 420 425 430	1296
gga acc agc ggt ctt cac atg gac tgg cct gta gtt tgc cca gtt tac Gly Thr Ser Gly Leu His Met Asp Trp Pro Val Val Cys Pro Val Tyr 435 440 445	1344
cct att aga gat tcg att ttt gga tcc tac gac gac caa aag gac gaa Pro Ile Arg Asp Ser Ile Phe Gly Ser Tyr Asp Asp Gln Lys Asp Glu 450 455 460	1392
tgt gtt cca att gag ccg ata ttt gag gag gag gct gaa gat tat gag Cys Val Pro Ile Glu Pro Ile Phe Glu Glu Glu Ala Glu Asp Tyr Glu 465 470 475 480	1440
gca tgt gcc aag ata att ttc gag tat tct cca agt gat gtt gat att Ala Cys Ala Lys Ile Ile Phe Glu Tyr Ser Pro Ser Asp Val Asp Ile 485 490 495	1488
agc aca aat aac cag aag ctt tca gac gtc gac ctt tac aag gag gcg Ser Thr Asn Asn Gln Lys Leu Ser Asp Val Asp Leu Tyr Lys Glu Ala 500 505 510	1536
atg aat aat gga aag ctg agc act gct ctt tca att atg ttt gct cct Met Asn Asn Gly Lys Leu Ser Thr Ala Leu Ser Ile Met Phe Ala Pro 515 520 525	1584
agg tac tct gag gat cgt ccg atc tat act aaa ggt gtc ggt ata aac Arg Tyr Ser Glu Asp Arg Pro Ile Tyr Thr Lys Gly Val Gly Ile Asn 530 535 540	1632
tgg gct aca tac tcc gtc gag gaa aag aaa tgt aac att ctc gac gtt Trp Ala Thr Tyr Ser Val Glu Glu Lys Lys Cys Asn Ile Leu Asp Val 545 550 555 560	1680
gtt ccc agc tgt ctt att ata agt aac ggc cac tat gcc ctt aca agt Val Pro Ser Cys Leu Ile Ile Ser Asn Gly His Tyr Ala Leu Thr Ser 565 570 575	1728
ctc agc tca ccc aat gaa gag gat gct ata aat tac ccc tgc gat atc	1776

Substitute Sequence Listing

Leu Ser Ser Pro Asn Glu Glu Asp Ala Ile Asn Tyr Pro Cys Asp Ile			
580	585	590	
gtt cag ggc aag ggg ttt ttg aag aac cca aac ggt gga aaa aag aat			1824
Val Gln Gly Lys Gly Phe Leu Lys Asn Pro Asn Gly Gly Lys Lys Asn			
595	600	605	
gct cag gaa ccg ccc aag gaa cct gaa cct gaa gaa cct aag aag gag			1872
Ala Gln Glu Pro Pro Lys Glu Pro Glu Pro Glu Glu Pro Lys Lys Glu			
610	615	620	
ggt gct gaa aac aaa ccc aaa gag aaa ggt aaa tct gag aaa aag aat			1920
Gly Ala Glu Asn Lys Pro Lys Glu Lys Gly Lys Ser Glu Lys Lys Asn			
625	630	635	640
gaa aaa tct atg cct tca gga cca ttc acg cca tac act agc ttg aag			1968
Glu Lys Ser Met Pro Ser Gly Pro Phe Thr Pro Tyr Thr Ser Leu Lys			
645	650	655	
aag gag ggt ttc gag tgc agt aaa tac act gtt gag cggt gta aac aaa			2016
Lys Glu Gly Phe Glu Cys Ser Lys Tyr Thr Val Glu Arg Val Asn Lys			
660	665	670	
agc tgc ggc gtt tac tat gaa tgc tca gaa acg cct gta tta ttt acc			2064
Ser Cys Gly Val Tyr Tyr Glu Cys Ser Glu Thr Pro Val Leu Phe Thr			
675	680	685	
aag aag aat agg att tat cta tac atc ata ttg gca gta tcg ctt gta			2112
Lys Lys Asn Arg Ile Tyr Leu Tyr Ile Ile Leu Ala Val Ser Leu Val			
690	695	700	
gta ctg gcc gtc tta gcc tac ttt gga tac agg tac tac agt aag aat			2160
Val Leu Ala Val Leu Ala Tyr Phe Gly Tyr Arg Tyr Ser Lys Asn			
705	710	715	720
cac ttg aaa aaa cac aat tcc cag ata tat gaa gat gat aac gtg aac			2208
His Leu Lys Lys His Asn Ser Gln Ile Tyr Glu Asp Asp Asn Val Asn			
725	730	735	
aac tac tac aat gag gac ttt gat gac gaa caa gat cggt gat gaa tac			2256
Asn Tyr Tyr Asn Glu Asp Phe Asp Asp Glu Gln Asp Arg Asp Glu Tyr			
740	745	750	
gct tcg aat gtt aga ggt gat caa atc tgg agc aga cac act cca gac			2304
Ala Ser Asn Val Arg Gly Asp Gln Ile Trp Ser Arg His Thr Pro Asp			
755	760	765	
aga tct gaa gtt act cca gtc aga atc tct agg tta aac cat taa			2349
Arg Ser Glu Val Thr Pro Val Arg Ile Ser Arg Leu Asn His			
770	775	780	

<210> 4
<211> 782
<212> PRT
<213> Theileria annulata

<400> 4

Met Lys Lys Ile Gly Leu Lys Ile Arg Ala Gln Lys Asp Lys Leu Asn
1 5 10 15

Substitute Sequence Listing

Pro Val Leu Gly Ser Asn Ser Asp Pro Ser Glu Glu Tyr Asp Ser Phe
20 25 30

Gln Gln Asn Val Phe Thr His Gln Pro Thr Gln Leu His Lys Ser His
35 40 45

His Tyr Ile Thr His Gln Lys Lys Thr Ser Gln His Ile Asp Asp Leu
50 55 60

Asn Phe Tyr Asn Gly Lys Phe Asn Gln Lys Ser Arg Ile Gly Pro Gly
65 70 75 80

Lys Val Val Asn Asn Ser Arg Asn Leu Val Glu Gly Glu Thr Leu Ser
85 90 95

Lys Asp Asp Asn Lys Thr Lys Ser Lys Ile Lys Ser Lys Thr Ala Ser
100 105 110

Ile Leu Pro Arg Leu Leu Lys Ser Leu Ser Phe Leu Ala Val Leu Gly
115 120 125

Ser Ile Asn Ser Phe Ser Leu Ala Leu Glu Glu Pro Phe Thr Gln His
130 135 140

Thr Ser Asn Arg Thr Pro Phe Glu Val Ser Leu Ile Gln Ser Asn Ser
145 150 155 160

Ser Leu Ser Pro Ile His Asn Ser Ser Thr Gln Asn Ser Ser His His
165 170 175

Asn Gly Phe Ser Gly Ser Thr Val Asn Asn Thr Ser Leu Ile Glu Thr
180 185 190

Arg Asn Asn Val Leu Asn Arg Thr Leu Gly Arg Phe Gly Ser Phe Leu
195 200 205

Gln Ser Gly Leu Ile Ser Ser Arg Ala Asp Lys Lys Lys Arg Ser Gly
210 215 220

Met Asn Arg Arg Gly Pro Lys Gly Lys Lys Gly Lys Gly Glu Asp
225 230 235 240

Glu Glu Lys Arg Asn Lys Trp Thr Asp Phe Met Ala Lys Phe Asp Ile
245 250 255

Ala Lys Val His Gly Ser Gly Val Tyr Val Asp Leu Gly Glu Ser Ala
260 265 270

Substitute Sequence Listing

Thr Val Gly Ser Tyr Asp Tyr Arg Met Pro Ile Gly Lys Cys Pro Val
275 280 285

Val Gly Lys Ala Ile Ile Leu Glu Asn Gly Ala Asp Phe Leu Ser Ser
290 295 300

Ile Thr His His Asp Pro Lys Glu Arg Gly Leu Gly Phe Pro Ala Thr
305 310 315 320

Lys Val Ala Ser Asn Ser Ser Lys Leu Asp Met Glu Asn Gln Leu Leu
325 330 335

Ser Pro Ile Ser Ala Gln Val Leu Arg Ser Trp Asn Tyr Lys His Glu
340 345 350

Ser Asp Leu Ser Asn Cys Ala Glu Tyr Ser Arg Asn Ile Val Pro Gly
355 360 365

Ser Asn Arg Asn Ser Lys Tyr Arg Tyr Pro Phe Val Tyr Asp Glu Ser
370 375 380

Glu Lys Leu Cys Tyr Ile Leu Tyr Ser Pro Met Gln Tyr Asn Gln Gly
385 390 395 400

Val Lys Tyr Cys Asp Gln Asp Ser Pro Asp Glu Gly Thr Ser Ser Leu
405 410 415

Ala Cys Met Tyr Pro Asp Lys Ser Lys Glu Asp Ser His Leu Phe Tyr
420 425 430

Gly Thr Ser Gly Leu His Met Asp Trp Pro Val Val Cys Pro Val Tyr
435 440 445

Pro Ile Arg Asp Ser Ile Phe Gly Ser Tyr Asp Asp Gln Lys Asp Glu
450 455 460

Cys Val Pro Ile Glu Pro Ile Phe Glu Glu Ala Glu Asp Tyr Glu
465 470 475 480

Ala Cys Ala Lys Ile Ile Phe Glu Tyr Ser Pro Ser Asp Val Asp Ile
485 490 495

Ser Thr Asn Asn Gln Lys Leu Ser Asp Val Asp Leu Tyr Lys Glu Ala
500 505 510

Met Asn Asn Gly Lys Leu Ser Thr Ala Leu Ser Ile Met Phe Ala Pro
515 520 525

Substitute Sequence Listing

Arg Tyr Ser Glu Asp Arg Pro Ile Tyr Thr Lys Gly Val Gly Ile Asn
530 535 540

Trp Ala Thr Tyr Ser Val Glu Glu Lys Lys Cys Asn Ile Leu Asp Val
545 550 555 560

Val Pro Ser Cys Leu Ile Ile Ser Asn Gly His Tyr Ala Leu Thr Ser
565 570 575

Leu Ser Ser Pro Asn Glu Glu Asp Ala Ile Asn Tyr Pro Cys Asp Ile
580 585 590

Val Gln Gly Lys Gly Phe Leu Lys Asn Pro Asn Gly Gly Lys Lys Asn
595 600 605

Ala Gln Glu Pro Pro Lys Glu Pro Glu Pro Glu Glu Pro Lys Lys Glu
610 615 620

Gly Ala Glu Asn Lys Pro Lys Glu Lys Gly Lys Ser Glu Lys Lys Asn
625 630 635 640

Glu Lys Ser Met Pro Ser Gly Pro Phe Thr Pro Tyr Thr Ser Leu Lys
645 650 655

Lys Glu Gly Phe Glu Cys Ser Lys Tyr Thr Val Glu Arg Val Asn Lys
660 665 670

Ser Cys Gly Val Tyr Tyr Glu Cys Ser Glu Thr Pro Val Leu Phe Thr
675 680 685

Lys Lys Asn Arg Ile Tyr Leu Tyr Ile Ile Leu Ala Val Ser Leu Val
690 695 700

Val Leu Ala Val Leu Ala Tyr Phe Gly Tyr Arg Tyr Tyr Ser Lys Asn
705 710 715 720

His Leu Lys Lys His Asn Ser Gln Ile Tyr Glu Asp Asp Asn Val Asn
725 730 735

Asn Tyr Tyr Asn Glu Asp Phe Asp Asp Glu Gln Asp Arg Asp Glu Tyr
740 745 750

Ala Ser Asn Val Arg Gly Asp Gln Ile Trp Ser Arg His Thr Pro Asp
755 760 765

Arg Ser Glu Val Thr Pro Val Arg Ile Ser Arg Leu Asn His

770

775 Substitute Sequence Listing
 780

<210> 5
<211> 1968
<212> DNA
<213> Babesia bovis

<220>
<221> CDS
<222> (1)..(1968)

Substitute Sequence Listing

Glu	Cys	Arg	Gly	Ile	Val	Gly	Cys	Asp	Gly	Ile	Met	Asp	Cys	Pro	Met
195							200							205	
ttc	aag	cag	acc	aac	tgg	aag	gat	atc	atg	ggc	ctc	ttt	aac	agt	tta
Phe	Lys	Gln	Thr	Asn	Trp	Lys	Asp	Ile	Met	Gly	Leu	Phe	Asn	Ser	Leu
210						215					220				
atg	aag	gag	gta	tgt	gat	att	tta	cct	cag	gac	gct	gtt	tgt	gag	cct
Met	Lys	Glu	Val	Cys	Asp	Ile	Leu	Pro	Gln	Asp	Ala	Val	Cys	Glu	Pro
225						230				235				240	
gta	tgg	gca	gaa	tgg	tca	tct	tgt	aac	ggg	gaa	tgt	ggc	gtt	cct	ggt
Val	Trp	Ala	Glu	Trp	Ser	Ser	Cys	Asn	Gly	Glu	Cys	Gly	Val	Pro	Gly
245						250				255					
aaa	cga	act	cgt	gct	ctt	ttg	gac	ctc	cga	atg	att	gaa	aag	ccc	gta
Lys	Arg	Thr	Arg	Ala	Leu	Leu	Asp	Leu	Arg	Met	Ile	Glu	Lys	Pro	Val
260						265					270				
aat	ggc	tcg	aat	gga	caa	ccg	ggt	aaa	tca	tgt	gag	gat	cag	aag	atg
Asn	Gly	Ser	Asn	Gly	Gln	Pro	Gly	Lys	Ser	Cys	Glu	Asp	Gln	Lys	Met
275						280					285				
aac	ttc	tta	ccc	caa	tca	gag	aca	tgc	acc	ata	gaa	tgc	aat	cat	gag
Asn	Phe	Leu	Pro	Gln	Ser	Glu	Thr	Cys	Thr	Ile	Glu	Cys	Asn	His	Glu
290						295				300					
cct	gtg	cca	agc	tcg	ccg	gaa	cct	gta	tca	gat	gat	atg	gat	cac	cca
Pro	Val	Pro	Ser	Ser	Pro	Glu	Pro	Val	Ser	Asp	Asp	Met	Asp	His	Pro
305						310				315				320	
gaa	cca	act	cct	gtt	aca	ccg	gaa	ggt	gac	atg	gat	aaa	tct	cat	tcc
Glu	Pro	Thr	Pro	Val	Thr	Pro	Glu	Gly	Asp	Met	Asp	Lys	Ser	His	Ser
325						330				335					
cat	tcg	agc	att	cca	tcc	acc	cct	gat	atg	cca	tca	agt	cac	agt	gat
His	Ser	Ser	Ile	Pro	Ser	Thr	Pro	Asp	Met	Pro	Ser	Ser	His	Ser	Asp
340						345				350					
atg	tca	tca	agc	cct	act	gat	atg	tca	tca	agc	cct	act	gac	atg	tca
Met	Ser	Ser	Pro	Thr	Asp	Met	Ser	Ser	Ser	Pro	Thr	Asp	Met	Ser	
355						360				365					
tca	agc	cct	act	gac	atg	tca	tca	agt	cac	agt	gac	atg	cca	tca	act
Ser	Ser	Pro	Thr	Asp	Met	Ser	Ser	His	Ser	Asp	Met	Pro	Ser	Thr	
370						375				380					
cct	act	ggc	atg	tca	tca	agt	cac	agt	gat	atg	cca	tca	agt	cac	agt
Pro	Thr	Gly	Met	Ser	Ser	His	Ser	Asp	Met	Pro	Ser	Ser	His	Ser	
385						390				395				400	
gat	atg	cca	tca	agc	cac	agt	gat	atg	tca	tca	agc	cct	act	gac	atg
Asp	Met	Pro	Ser	Ser	His	Ser	Asp	Met	Ser	Ser	Ser	Pro	Thr	Asp	Met
405						410				415					
tca	tca	agt	cac	gct	gat	act	cgt	gta	gga	aat	acc	gat	gaa	gaa	cat
Ser	Ser	Ser	His	Ala	Asp	Thr	Arg	Val	Gly	Asn	Thr	Asp	Glu	Glu	His
420						425				430					
aac	cac	agg	aaa	gat	atg	gat	gtc	aag	ttc	ccc	gaa	aat	atg	gat	gat
Asn	His	Arg	Lys	Asp	Met	Asp	Val	Lys	Phe	Pro	Glu	Asn	Met	Asp	Asp
435						440				445					

Substitute Sequence Listing

atc cca gtc gag gat aat cct ata ccc aca gat cct aga cat ggc gtc Ile Pro Val Glu Asp Asn Pro Ile Pro Thr Asp Pro Arg His Gly Val 450 455 460	1392
gaa cca tcg cct tct gat gtg atc cct gag gat gac caa ctt cgt agg Glu Pro Ser Pro Ser Asp Val Ile Pro Glu Asp Asp Gln Leu Arg Arg 465 470 475 480	1440
acg ctt gaa atg cag cgc gaa gag gac cta aag aag gaa ttg atg ctc Thr Leu Glu Met Gln Arg Glu Glu Asp Leu Lys Lys Glu Leu Met Leu 485 490 495	1488
caa cat gaa ctg aag ctt cag gaa gaa aag gaa agg gca gct att tta Gln His Glu Leu Lys Leu Gln Glu Glu Lys Glu Arg Ala Ala Ile Leu 500 505 510	1536
gag aat aac act cct tat gga tcc gcc act tcc gtg tcg caa gac ggt Glu Asn Asn Thr Pro Tyr Gly Ser Ala Thr Ser Val Ser Gln Asp Gly 515 520 525	1584
gaa tct cca act ggc gta ccc caa agt agc gag acc gat gca ata cgt Glu Ser Pro Thr Gly Val Pro Gln Ser Ser Glu Thr Asp Ala Ile Arg 530 535 540	1632
cac gag gtg tat gac gat cac ccc gag gaa tct gaa aac acc ggg att His Glu Val Tyr Asp His Pro Glu Glu Ser Glu Asn Thr Gly Ile 545 550 555 560	1680
aat gct gat gtg acc gaa tct gag gac tat gag ggt gaa aaa caa aag Asn Ala Asp Val Thr Glu Ser Glu Asp Tyr Glu Gly Glu Lys Gln Lys 565 570 575	1728
gac gaa tca aat gaa cgt tcg acc agc aac act act aag att gcc ggc Asp Glu Ser Asn Glu Arg Ser Thr Ser Asn Thr Thr Lys Ile Ala Gly 580 585 590	1776
ggt gct cta cta ggt ctt ctt ctc ctt ggt gcc ggt ggt gga tac gct Gly Ala Leu Leu Gly Leu Leu Leu Gly Ala Gly Gly Gly Tyr Ala 595 600 605	1824
atg tac aaa aag aac aag aca cct act gtt gag aca ggt tca ggt gat Met Tyr Lys Lys Asn Lys Thr Pro Thr Val Glu Thr Gly Ser Gly Asp 610 615 620	1872
tac act ggg gcc gac gag agt tca gaa ccc atg aag gag ggt gac aca Tyr Thr Gly Ala Asp Glu Ser Ser Glu Pro Met Lys Glu Gly Asp Thr 625 630 635 640	1920
tac acc gtc act gag ttt gac aac aac att tgg ggc gag gca gcg taa Tyr Thr Val Thr Glu Phe Asp Asn Asn Ile Trp Gly Glu Ala Ala 645 650 655	1968

<210> 6
<211> 655
<212> PRT
<213> Babesia bovis

<400> 6

Met Ile Gly Tyr Ile Lys Ile Leu Ala Ser Val Pro Leu Leu Ser Leu
1 5 10 15

Substitute Sequence Listing

Ala Phe Leu Ala Thr Thr Gly Ile His Ala Phe Ala Asp Lys Gly Ile
20 25 30

Gly Ser Pro Lys Gly Lys Gln Cys Lys Lys Gln Leu Asp Phe Ser Ile
35 40 45

Val Val Asp Glu Ser Ala Ser Ile Ser Asp Asp Gln Trp Glu Gly Gln
50 55 60

Met Ile Pro Phe Leu Arg Asn Leu Ile His Thr Val Asp Leu Asp Asn
65 70 75 80

Thr Asp Ile Arg Leu Ser Leu Thr Thr Tyr Ser Thr Pro Thr Arg Gln
85 90 95

Ile Phe Thr Phe Leu Asp Ala Ala Ser Ser Thr Arg Leu Ala Leu
100 105 110

Thr Lys Leu Asp Trp Met Asn Gly Thr Lys Ala Arg Tyr Gly Met Thr
115 120 125

Tyr Thr Gly Arg Ala Leu Asn Tyr Val Arg Lys Ala Ile Leu Pro Tyr
130 135 140

Gly Arg Lys Asn Val Pro Lys Ala Leu Leu Ile Thr Asp Gly Val
145 150 155 160

Ser Ser Asp Gly Ser Tyr Thr Ala Gln Val Ala Ala Met Leu Arg Asp
165 170 175

Glu Gly Val Asn Val Met Val Ile Gly Val Gly Asp Val Asn Val Ala
180 185 190

Glu Cys Arg Gly Ile Val Gly Cys Asp Gly Ile Met Asp Cys Pro Met
195 200 205

Phe Lys Gln Thr Asn Trp Lys Asp Ile Met Gly Leu Phe Asn Ser Leu
210 215 220

Met Lys Glu Val Cys Asp Ile Leu Pro Gln Asp Ala Val Cys Glu Pro
225 230 235 240

Val Trp Ala Glu Trp Ser Ser Cys Asn Gly Glu Cys Gly Val Pro Gly
245 250 255

Lys Arg Thr Arg Ala Leu Leu Asp Leu Arg Met Ile Glu Lys Pro Val
260 265 270

Substitute Sequence Listing

Asn Gly Ser Asn Gly Gln Pro Gly Lys Ser Cys Glu Asp Gln Lys Met
275 280 285

Asn Phe Leu Pro Gln Ser Glu Thr Cys Thr Ile Glu Cys Asn His Glu
290 295 300

Pro Val Pro Ser Ser Pro Glu Pro Val Ser Asp Asp Met Asp His Pro
305 310 315 320

Glu Pro Thr Pro Val Thr Pro Glu Gly Asp Met Asp Lys Ser His Ser
325 330 335

His Ser Ser Ile Pro Ser Thr Pro Asp Met Pro Ser Ser His Ser Asp
340 345 350

Met Ser Ser Ser Pro Thr Asp Met Ser Ser Ser Pro Thr Asp Met Ser
355 360 365

Ser Ser Pro Thr Asp Met Ser Ser Ser His Ser Asp Met Pro Ser Thr
370 375 380

Pro Thr Gly Met Ser Ser Ser His Ser Asp Met Pro Ser Ser His Ser
385 390 395 400

Asp Met Pro Ser Ser His Ser Asp Met Ser Ser Ser Pro Thr Asp Met
405 410 415

Ser Ser Ser His Ala Asp Thr Arg Val Gly Asn Thr Asp Glu Glu His
420 425 430

Asn His Arg Lys Asp Met Asp Val Lys Phe Pro Glu Asn Met Asp Asp
435 440 445

Ile Pro Val Glu Asp Asn Pro Ile Pro Thr Asp Pro Arg His Gly Val
450 455 460

Glu Pro Ser Pro Ser Asp Val Ile Pro Glu Asp Asp Gln Leu Arg Arg
465 470 475 480

Thr Leu Glu Met Gln Arg Glu Glu Asp Leu Lys Lys Glu Leu Met Leu
485 490 495

Gln His Glu Leu Lys Leu Gln Glu Glu Lys Glu Arg Ala Ala Ile Leu
500 505 510

Glu Asn Asn Thr Pro Tyr Gly Ser Ala Thr Ser Val Ser Gln Asp Gly
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515

Substitute Sequence Listing
520 525

Glu Ser Pro Thr Gly Val Pro Gln Ser Ser Glu Thr Asp Ala Ile Arg
530 535 540

His Glu Val Tyr Asp Asp His Pro Glu Glu Ser Glu Asn Thr Gly Ile
545 550 555 560

Asn Ala Asp Val Thr Glu Ser Glu Asp Tyr Glu Gly Glu Lys Gln Lys
565 570 575

Asp Glu Ser Asn Glu Arg Ser Thr Ser Asn Thr Thr Lys Ile Ala Gly
580 585 590

Gly Ala Leu Leu Gly Leu Leu Leu Leu Gly Ala Gly Gly Gly Tyr Ala
595 600 605

Met Tyr Lys Lys Asn Lys Thr Pro Thr Val Glu Thr Gly Ser Gly Asp
610 615 620

Tyr Thr Gly Ala Asp Glu Ser Ser Glu Pro Met Lys Glu Gly Asp Thr
625 630 635 640

Tyr Thr Val Thr Glu Phe Asp Asn Asn Ile Trp Gly Glu Ala Ala
645 650 655

<210> 7

<211> 1047

<212> DNA

<213> Theileria annulata

<220>

<221> CDS

<222> (1)..(1047)

<400> 7

gat aag ggg cta tat cct gac ggt ata aag aaa ccg agc tcc tac tgc	48
Asp Lys Gly Leu Tyr Pro Asp Gly Ile Lys Lys Pro Ser Ser Tyr Cys	
1 5 10 15	

cac agg gaa ttg gac tta aca ata tta gtc gat gaa tcc tcg agt atc	96
His Arg Glu Leu Asp Leu Thr Ile Leu Val Asp Glu Ser Ser Ser Ile	
20 25 30	

tat att gaa gag tgg aac aaa ctc att cca ttt ctt aaa tca ctg gtg	144
Tyr Ile Glu Glu Trp Asn Lys Leu Ile Pro Phe Leu Lys Ser Leu Val	
35 40 45	

aga tca ata aat ata agt cca aat tat gtg cac ttg tca atg gtc acc	192
Arg Ser Ile Asn Ile Ser Pro Asn Tyr Val His Leu Ser Met Val Thr	
50 55 60	

ttt tcc act tca att cggtgg tta ata tca ttt ctc gac cca gcc tct	240
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Substitute Sequence Listing

Phe Ser Thr Ser Ile Arg Trp Leu Ile Ser Phe Leu Asp Pro Ala Ser				
65	70	75	80	
aag gat gag caa ttg gcc ctt gct gtt ctg gac aag ctg aag aac agt				288
Lys Asp Glu Gln Leu Ala Leu Ala Val Leu Asp Lys Leu Lys Asn Ser				
85	90	95		
aag cct gtg ttt ggg tac aca ttc act gga cag gca ctt aac ttt att				336
Lys Pro Val Phe Gly Tyr Thr Phe Thr Gly Gln Ala Leu Asn Phe Ile				
100	105	110		
tct gag gct gtt tat atg ttt ggt gct agg cgt aac tct cca aag ggc				384
Ser Glu Ala Val Tyr Met Phe Gly Ala Arg Arg Asn Ser Pro Lys Gly				
115	120	125		
atc att atc atc acc gac gga tcc tct act cag aca aac gtt act tct				432
Ile Ile Ile Ile Thr Asp Gly Ser Ser Thr Gln Thr Asn Val Thr Ser				
130	135	140		
cag gcg tcg gct cta cta agg gat gct ggt gta aca att cta gtt gtt				480
Gln Ala Ser Ala Leu Leu Arg Asp Ala Gly Val Thr Ile Leu Val Val				
145	150	155	160	
gga gtt ggg aag gct aaa gaa agc gag tgt aga ggt ata gtt ggt tgt				528
Gly Val Gly Lys Ala Lys Glu Ser Glu Cys Arg Gly Ile Val Gly Cys				
165	170	175		
tct acc aaa gga gag tgc ccc ctt ttc ttt atg acc aac tgg gat gaa				576
Ser Thr Lys Gly Glu Cys Pro Leu Phe Phe Met Thr Asn Trp Asp Glu				
180	185	190		
att atc agg aag gtt ggg gag ttg atg gct gag gtt tgt gag acc att				624
Ile Ile Arg Lys Val Gly Glu Leu Met Ala Glu Val Cys Glu Thr Ile				
195	200	205		
cct aag gac gcc gta tgt aag ccg atc tgg tct gat tgg tct aag tgt				672
Pro Lys Asp Ala Val Cys Lys Pro Ile Trp Ser Asp Trp Ser Lys Cys				
210	215	220		
gac gcc aag tgc ggc att ggg acg agg tac caa aag ttg atg gga gtt				720
Asp Ala Lys Cys Gly Ile Gly Thr Arg Tyr Gln Lys Leu Met Gly Val				
225	230	235	240	
act aca att tct gag cca act gtc gga acg aac ggc aag tcc ggg agg				768
Thr Thr Ile Ser Glu Pro Thr Val Gly Thr Asn Gly Lys Ser Gly Arg				
245	250	255		
aca tgt gag atg att tat gag aac gtc gag gtt cca aag gag gag tgc				816
Thr Cys Glu Met Ile Tyr Glu Asn Val Glu Val Pro Lys Glu Glu Cys				
260	265	270		
tcc gtt gag tct aag att gct gga gga gtg gct cta gca ctg tta atg				864
Ser Val Glu Ser Lys Ile Ala Gly Gly Val Ala Leu Ala Leu Leu Met				
275	280	285		
ctt gca ggc gga ggt ggt tac aca tac tac aaa aag tac ggt tta tct				912
Leu Ala Gly Gly Gly Tyr Thr Tyr Tyr Lys Lys Tyr Gly Leu Ser				
290	295	300		
aga gtg agt gaa act acg aat ttg gat gag gat ttt gca gat tct agt				960
Arg Val Ser Glu Thr Thr Asn Leu Asp Glu Asp Phe Ala Asp Ser Ser				
305	310	315	320	

Substitute Sequence Listing

ggg aac cgt ggt gta agg gag agt gtg ggt gaa gct tac aca gta act	1008
Gly Asn Arg Gly Val Arg Glu Ser Val Gly Glu Ala Tyr Thr Val Thr	
325 330 335	
gat tta gat gat gga ctc tgg agc caa tcc aat caa taa	1047
Asp Leu Asp Asp Gly Leu Trp Ser Gln Ser Asn Gln	
340 345	
<210> 8	
<211> 348	
<212> PRT	
<213> Theileria annulata	
<400> 8	
Asp Lys Gly Leu Tyr Pro Asp Gly Ile Lys Lys Pro Ser Ser Tyr Cys	
1 5 10 15	
His Arg Glu Leu Asp Leu Thr Ile Leu Val Asp Glu Ser Ser Ser Ile	
20 25 30	
Tyr Ile Glu Glu Trp Asn Lys Leu Ile Pro Phe Leu Lys Ser Leu Val	
35 40 45	
Arg Ser Ile Asn Ile Ser Pro Asn Tyr Val His Leu Ser Met Val Thr	
50 55 60	
Phe Ser Thr Ser Ile Arg Trp Leu Ile Ser Phe Leu Asp Pro Ala Ser	
65 70 75 80	
Lys Asp Glu Gln Leu Ala Leu Ala Val Leu Asp Lys Leu Lys Asn Ser	
85 90 95	
Lys Pro Val Phe Gly Tyr Thr Phe Thr Gly Gln Ala Leu Asn Phe Ile	
100 105 110	
Ser Glu Ala Val Tyr Met Phe Gly Ala Arg Arg Asn Ser Pro Lys Gly	
115 120 125	
Ile Ile Ile Ile Thr Asp Gly Ser Ser Thr Gln Thr Asn Val Thr Ser	
130 135 140	
Gln Ala Ser Ala Leu Leu Arg Asp Ala Gly Val Thr Ile Leu Val Val	
145 150 155 160	
Gly Val Gly Lys Ala Lys Glu Ser Glu Cys Arg Gly Ile Val Gly Cys	
165 170 175	
Ser Thr Lys Gly Glu Cys Pro Leu Phe Phe Met Thr Asn Trp Asp Glu	
180 185 190	

Substitute Sequence Listing

Ile Ile Arg Lys Val Gly Glu Leu Met Ala Glu Val Cys Glu Thr Ile
195 200 205

Pro Lys Asp Ala Val Cys Lys Pro Ile Trp Ser Asp Trp Ser Lys Cys
210 215 220

Asp Ala Lys Cys Gly Ile Gly Thr Arg Tyr Gln Lys Leu Met Gly Val
225 230 235 240

Thr Thr Ile Ser Glu Pro Thr Val Gly Thr Asn Gly Lys Ser Gly Arg
245 250 255

Thr Cys Glu Met Ile Tyr Glu Asn Val Glu Val Pro Lys Glu Glu Cys
260 265 270

Ser Val Glu Ser Lys Ile Ala Gly Gly Val Ala Leu Ala Leu Leu Met
275 280 285

Leu Ala Gly Gly Gly Tyr Thr Tyr Tyr Lys Lys Tyr Gly Leu Ser
290 295 300

Arg Val Ser Glu Thr Thr Asn Leu Asp Glu Asp Phe Ala Asp Ser Ser
305 310 315 320

Gly Asn Arg Gly Val Arg Glu Ser Val Gly Glu Ala Tyr Thr Val Thr
325 330 335

Asp Leu Asp Asp Gly Leu Trp Ser Gln Ser Asn Gln
340 345

<210> 9

<211> 2259

<212> DNA

<213> Babesia bovis

<220>

<221> CDS

<222> (552)..(2189)

<220>

<221> misc_feature

<222> (1465)..(1465)

<223> The 'r' at location 1465 stands for g or a

<400> 9

ataagatgt a gactgatgt gtgtactcg gg actctgacac tggaggatag gctaccagaa 60

ctgggcgcaa ctcccta atg gagtgccgct cccaggaggc cacagaacaa tggagtacaa 120

cgctcaaaac cgca gatgt aat gttatgtacat attgtcatgg agttcgtaat 180

Substitute Sequence Listing

cctaacaag gccattgtat cgtcaatgtg gtctaccagt ggacgtcgct tggaggcc	240
agggtacatc aaatccctga gaacacctat cgtccggtgt tacggtgta atgggttact	300
ataaaaagcaa atttaattgt agatattgt aaaaaactgt aaaattggtt agtgcttgca	360
ccgtccctggc cccgcgattt ggataccgct gtgctacgct ttgcacggaa tcacgacgtc	420
gtgcataacg ctgtgcttat gacttcgtac acatcaaacg acttaactg ccgttggttt	480
ataacgttg gcgttaggtt gttttgggtg ttattgtact gtggaatcat acacattcta	540
cacgtgtcat g atg gtg aag ttc cac aca tta tcg gtt gca gcc atc ctg Met Val Lys Phe His Thr Leu Ser Val Ala Ala Ile Leu	590
1 5 10	
gcg att gct tca tcc aat act att ttt gct aca ttt aga tca aat gga Ala Ile Ala Ser Ser Asn Thr Ile Phe Ala Thr Phe Arg Ser Asn Gly	638
15 20 25	
aaa acc ttc gga gat gaa tct gtt agc ctt cta gaa cat gaa agt acc Lys Thr Phe Gly Asp Glu Ser Val Ser Leu Leu Glu His Glu Ser Thr	686
30 35 40 45	
agt ttg tct cgt ggt cct aga cca acc gaa gat caa atc agt cag tta Ser Leu Ser Arg Gly Pro Arg Pro Thr Glu Asp Gln Ile Ser Gln Leu	734
50 55 60	
cca aaa aat gtt ttc ttt cta ttg gat aac agc att gat atg tct att Pro Lys Asn Val Phe Phe Leu Leu Asp Asn Ser Ile Asp Met Ser Ile	782
65 70 75	
gaa act gga gaa gag aat cgt cat ttc ctc tcc gag ttt ttt aaa ttg Glu Thr Gly Glu Glu Asn Arg His Phe Leu Ser Glu Phe Phe Lys Leu	830
80 85 90	
tta aaa aaa tat gaa gga ata aat gtt tca cta ata agg tac aat agt Leu Lys Lys Tyr Glu Gly Ile Asn Val Ser Leu Ile Arg Tyr Asn Ser	878
95 100 105	
gaa gaa ccg tta ggt tcg acg aaa gca tta acc aac ggg gag ttg aaa Glu Glu Pro Leu Gly Ser Thr Lys Ala Leu Thr Asn Gly Glu Leu Lys	926
110 115 120 125	
aaa cta tcc gat aat att cct act aaa atg cct ttt gac att ggc gtt Lys Leu Ser Asp Asn Ile Pro Thr Lys Met Pro Phe Asp Ile Gly Val	974
130 135 140	
gtt cct act ggt ata gga gct gcc ctc aaa cag ata aaa aca ttg tac Val Pro Thr Gly Ile Gly Ala Ala Leu Lys Gln Ile Lys Thr Leu Tyr	1022
145 150 155	
cct gat cac gaa aag ttc ctt gtt ggg aac acc att act gag ttg gat Pro Asp His Glu Lys Phe Leu Val Gly Asn Thr Ile Thr Glu Leu Asp	1070
160 165 170	
tat tct aaa gca ttg ggt aag gat att gtt gta atc gtg ttt act act Tyr Ser Lys Ala Leu Gly Lys Asp Ile Val Val Ile Val Phe Thr Thr	1118
175 180 185	
ggc cac gtc att gat cca tat tta gca tat gat gag gca ttt gat gcc Gly His Val Ile Asp Pro Tyr Leu Ala Tyr Asp Glu Ala Phe Asp Ala	1166
190 195 200 205	

Substitute Sequence Listing

cgc cgt aat ggt gta aga ttt tac gtt att aat agg gga gga aag gca Arg Arg Asn Gly Val Arg Phe Tyr Val Ile Asn Arg Gly Gly Lys Ala 210 215 220	1214
aaa aac tat tgg act cag cta ttg gga tgc cac tac aat act tgt ttg Lys Asn Tyr Trp Thr Gln Leu Leu Gly Cys His Tyr Asn Thr Cys Leu 225 230 235	1262
agt tat att cgg gcc aaa ata aca agg cct tca cta tat ctc gat gtt Ser Tyr Ile Arg Ala Lys Ile Thr Arg Pro Ser Leu Tyr Leu Asp Val 240 245 250	1310
ttg gtg aac agg att gtg tct aaa cgc gcg aaa gat gcc gtt tgt ttg Leu Val Asn Arg Ile Val Ser Lys Arg Ala Lys Asp Ala Val Cys Leu 255 260 265	1358
gaa gtg tgg acg gat tat aaa cct aac act gaa aaa tcg gat gtg agg Glu Val Trp Thr Asp Tyr Lys Pro Asn Thr Glu Lys Ser Asp Val Arg 270 275 280 285	1406
att atg act tct acg ttg aaa tta tac aaa acc ctt ctt act gga agc Ile Met Thr Ser Thr Leu Lys Leu Tyr Lys Thr Leu Leu Thr Gly Ser 290 295 300	1454
ttt gcg gag ara aac atc aaa ggt ctc aca tgt gat gag cag cta aag Phe Ala Glu Xaa Asn Ile Lys Gly Leu Thr Cys Asp Glu Gln Leu Lys 305 310 315	1502
gat atg cag aaa aga caa ata ttt tgc tac tca aat aag tgt gct ccc Asp Met Gln Lys Arg Gln Ile Phe Cys Tyr Ser Asn Lys Cys Ala Pro 320 325 330	1550
acg atc tat tca aga tct tat gtt gac tta gct att caa cgt ctt aat Thr Ile Tyr Ser Arg Ser Tyr Val Asp Leu Ala Ile Gln Arg Leu Asn 335 340 345	1598
gca aaa gat ttt aaa gag gta cta gat gag tca tct tac aga tca cgc Ala Lys Asp Phe Lys Glu Val Leu Asp Glu Ser Ser Tyr Arg Ser Arg 350 355 360 365	1646
agt ttg caa tca gtg gag aaa cat aat gag caa caa aca ggt tct caa Ser Leu Gln Ser Val Glu Lys His Asn Glu Gln Gln Thr Gly Ser Gln 370 375 380	1694
gaa acg ctt tct gga agc gcc cgt gta gaa aca agc tta gaa agc tca Glu Thr Leu Ser Gly Ser Ala Arg Val Glu Thr Ser Leu Glu Ser Ser 385 390 395	1742
gta cct tca tcc tat gtg gca gaa ttg gga gaa agt gat aca gaa aca Val Pro Ser Ser Tyr Val Ala Glu Leu Gly Glu Ser Asp Thr Glu Thr 400 405 410	1790
tac aaa cag ttg gag tac ata gat aaa aat ggc gtc act gtc ttc aac Tyr Lys Gln Leu Glu Tyr Ile Asp Lys Asn Gly Val Thr Val Phe Asn 415 420 425	1838
gat gag ccc act gtt gtt gtc gat act ccc gag tac gta caa aag gtg Asp Glu Pro Thr Val Val Val Asp Thr Pro Glu Tyr Val Gln Lys Val 430 435 440 445	1886
cat gaa aga gaa atg cag ttt gat gaa gaa tcc acc cat ctt ccc aac His Glu Arg Glu Met Gln Phe Asp Glu Glu Ser Thr His Leu Pro Asn	1934

Substitute Sequence Listing
 450 455 460

tct ggt aac cac cat cca cct cat cac cga aag ggg gcc aac gga tcc Ser Gly Asn His His Pro Pro His His Arg Lys Gly Ala Asn Gly Ser 465 470 475	1982
ggt aaa aag acc acg atc gtc gtt ggt att ata tgc ctt gta gta ata Gly Lys Lys Thr Thr Ile Val Val Gly Ile Ile Cys Leu Val Val Ile 480 485 490	2030
tgc gcc gtc ata gcc ggc gcc tac cta tcc ctt tca cag caa gag tct Cys Ala Val Ile Ala Gly Ala Tyr Leu Ser Leu Ser Gln Gln Glu Ser 495 500 505	2078
gtg gaa ctc acc tct gaa gag ggt gac ttc ttg aac gac act acg ggt Val Glu Leu Thr Ser Glu Glu Gly Asp Phe Leu Asn Asp Thr Thr Gly 510 515 520 525	2126
ggt caa cct gag gta ctc gaa aca caa cag gtt gtg gat gca gag aac Gly Gln Pro Glu Val Leu Glu Thr Gln Gln Val Val Asp Ala Glu Asn 530 535 540	2174
aaa aca tgg ttg taa gacacgaaac gggttgtcac agccaacata tacaaatgca Lys Thr Trp Leu 545	2229
gtttaaatta agtcactagt taaaaaaaaa	2259

<210> 10
<211> 545
<212> PRT
<213> Babesia bovis

<220>
<221> misc_feature
<222> (305)..(305)
<223> The 'Xaa' at location 305 stands for Arg, or Lys.

<400> 10

Met Val Lys Phe His Thr Leu Ser Val Ala Ala Ile Leu Ala Ile Ala
 1 5 10 15

Ser Ser Asn Thr Ile Phe Ala Thr Phe Arg Ser Asn Gly Lys Thr Phe
 20 25 30

Gly Asp Glu Ser Val Ser Leu Leu Glu His Glu Ser Thr Ser Leu Ser
 35 40 45

Arg Gly Pro Arg Pro Thr Glu Asp Gln Ile Ser Gln Leu Pro Lys Asn
 50 55 60

Val Phe Phe Leu Leu Asp Asn Ser Ile Asp Met Ser Ile Glu Thr Gly
 65 70 75 80

Glu Glu Asn Arg His Phe Leu Ser Glu Phe Phe Lys Leu Leu Lys Lys
 85 90 95

Substitute Sequence Listing

Tyr Glu Gly Ile Asn Val Ser Leu Ile Arg Tyr Asn Ser Glu Glu Pro
100 105 110

Leu Gly Ser Thr Lys Ala Leu Thr Asn Gly Glu Leu Lys Lys Leu Ser
115 120 125

Asp Asn Ile Pro Thr Lys Met Pro Phe Asp Ile Gly Val Val Pro Thr
130 135 140

Gly Ile Gly Ala Ala Leu Lys Gln Ile Lys Thr Leu Tyr Pro Asp His
145 150 155 160

Glu Lys Phe Leu Val Gly Asn Thr Ile Thr Glu Leu Asp Tyr Ser Lys
165 170 175

Ala Leu Gly Lys Asp Ile Val Val Ile Val Phe Thr Thr Gly His Val
180 185 190

Ile Asp Pro Tyr Leu Ala Tyr Asp Glu Ala Phe Asp Ala Arg Arg Asn
195 200 205

Gly Val Arg Phe Tyr Val Ile Asn Arg Gly Gly Lys Ala Lys Asn Tyr
210 215 220

Trp Thr Gln Leu Leu Gly Cys His Tyr Asn Thr Cys Leu Ser Tyr Ile
225 230 235 240

Arg Ala Lys Ile Thr Arg Pro Ser Leu Tyr Leu Asp Val Leu Val Asn
245 250 255

Arg Ile Val Ser Lys Arg Ala Lys Asp Ala Val Cys Leu Glu Val Trp
260 265 270

Thr Asp Tyr Lys Pro Asn Thr Glu Lys Ser Asp Val Arg Ile Met Thr
275 280 285

Ser Thr Leu Lys Leu Tyr Lys Thr Leu Leu Thr Gly Ser Phe Ala Glu
290 295 300

Xaa Asn Ile Lys Gly Leu Thr Cys Asp Glu Gln Leu Lys Asp Met Gln
305 310 315 320

Lys Arg Gln Ile Phe Cys Tyr Ser Asn Lys Cys Ala Pro Thr Ile Tyr
325 330 335

Ser Arg Ser Tyr Val Asp Leu Ala Ile Gln Arg Leu Asn Ala Lys Asp

Substitute Sequence Listing
345 350

Phe Lys Glu Val Leu Asp Glu Ser Ser Tyr Arg Ser Arg Ser Leu Gln
 355 360 365

Ser Val Glu Lys His Asn Glu Gln Gln Thr Gly Ser Gln Glu Thr Leu
 370 375 380

Ser Gly Ser Ala Arg Val Glu Thr Ser Leu Glu Ser Ser Val Pro Ser
 385 390 395 400

Ser Tyr Val Ala Glu Leu Gly Glu Ser Asp Thr Glu Thr Tyr Lys Gln
 405 410 415

Leu Glu Tyr Ile Asp Lys Asn Gly Val Thr Val Phe Asn Asp Glu Pro
 420 425 430

Thr Val Val Val Asp Thr Pro Glu Tyr Val Gln Lys Val His Glu Arg
 435 440 445

Glu Met Gln Phe Asp Glu Glu Ser Thr His Leu Pro Asn Ser Gly Asn
 450 455 460

His His Pro Pro His His Arg Lys Gly Ala Asn Gly Ser Gly Lys Lys
 465 470 475 480

Thr Thr Ile Val Val Gly Ile Ile Cys Leu Val Val Ile Cys Ala Val
 485 490 495

Ile Ala Gly Ala Tyr Leu Ser Leu Ser Gln Gln Glu Ser Val Glu Leu
 500 505 510

Thr Ser Glu Glu Gly Asp Phe Leu Asn Asp Thr Thr Gly Gly Gln Pro
 515 520 525

Glu Val Leu Glu Thr Gln Gln Val Val Asp Ala Glu Asn Lys Thr Trp
 530 535 540

Leu
 545

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<211> 22
<212> DNA
<213> Artificial

<220>
<223> primer 1
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Substitute Sequence Listing

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<210> 12
<211> 24
<212> DNA
<213> Artificial

<220>
<223> primer 2

<400> 12 caaaaggata cctatatttgcgtac 24

<210> 13
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Primer 3

<400> 13 tgtggtagat gaatctgcta gtatatc 27

<210> 14
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Primer 4

<400> 14 ctatgccacg gcattcagca acattta 27

<210> 15
<211> 27
<212> DNA
<213> Artificial

<220>
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<400> 15 cccggatcca tgcagttaca taacaaa 27

<210> 16
<211> 27
<212> DNA
<213> Artificial

<220>
<223> Primer 6

<400> 16 ggaaagcttc tgagcaaagg aaatagg 27

Substitute Sequence Listing

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<212> DNA
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<220>
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27

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<212> DNA
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<210> 19
<211> 30
<212> DNA
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30

<210> 20
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Primer 10

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29